

SEQUENCE LISTING

<110> Soll, Dieter

<120> Glu-tRNA-Gln Amidotransferase- A Novel Essential
Translational Component

<130> 03818/0200029

<140> US 09/355,622

<141> 1999-09-23

<150> US 60/037,275

<151> 1997-02-03

<150> PCT/US 98/01860

<151> 1998-02-03

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<170> PatentIn Ver. 2.1

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<212> DNA

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 <222> (1)..(1458)
 <223> Subunit A, corresponds to nucleotides 409-1869 of
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 aaa aaa gag att aag att tct gat ctg gtt gat gaa tct tat aaa cgc 96

Lys	Lys	Glu	Ile	Lys	Ile	Ser	Asp	Leu	Val	Asp	Glu	Ser	Tyr	Lys	Arg	
20								25						30		
atc caa gcg gtt gat gat aag gta caa gcc ttt ttg gca tta gat gaa															144	
Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu																
35						40							45			
gaa aga gcg cgc gca tac gcg aag gag ctt gat gag gcg gtt gac ggc															192	
Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly																
50						55							60			
cgt tct gag cac ggt ctt ctt ttc ggt atg ccg atc ggc gta aaa gat															240	
Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp																
65						70							75		80	
aat atc gta aca aaa ggg ctg cgc aca aca tgc tcc agc aaa att ctc															288	
Asn Ile Val Thr Lys Gly Leu Arg Thr Thr Cys Ser Ser Lys Ile Leu																
85						90							95			
gaa aac ttt gat ccg att tac gat gct act gtc gtt cag cgc ctt caa															336	
Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr Val Val Gln Arg Leu Gln																
100						105							110			
gac gct gaa gcg gtc aca atc gga aaa ctg aac atg gac gaa ttc gcc															384	
Asp Ala Glu Ala Val Thr Ile Gly Lys Leu Asn Met Asp Glu Phe Ala																
115						120							125			
atg ggg tca tct aca gaa aac tca gct tac aag ctg acg aaa aac cct															432	
Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr Lys Leu Thr Lys Asn Pro																
130						135							140			
tgg aac ctg gat aca gtt ccc ggc ggt tca agc ggc gga tct gca gct															480	
Trp Asn Leu Asp Thr Val Pro Gly Gly Ser Ser Gly Gly Ser Ala Ala																
145						150							155		160	
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Ala Val Ala Ala Gly Glu Val Pro Phe Ser Leu Gly Ser Asp Thr Gly																
165						170							175			
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Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys Gly Val Val Gly Leu Lys																
180						185							190			
cct aca tac gga cgt gta tct cgt tac ggc ctg gtc gca ttt gcg tct															624	
Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser																
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tca ttg gac caa atc gga ccg att aca cgt acg gtt gag gat aac gcg															672	
Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg Thr Val Glu Asp Asn Ala																
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Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser																
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Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val			
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ggc aaa gaa gcg aga gaa tct gtc ttg gca gcg ctg aaa gtc ctt gaa			864
Gly Lys Glu Ala Arg Glu Ser Val Leu Ala Ala Leu Lys Val Leu Glu			
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Gly Leu Gly Ala Thr Trp Glu Glu Val Ser Leu Pro His Ser Lys Tyr			
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gcg ctt gcg aca tat tac ctg ctg tca tct tct gaa gcg tca gcg aac			960
Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser Glu Ala Ser Ala Asn			
305	310	315	320
ctt gca cgc ttt gac ggc atc cgc tac ggc tac cgc aca gac aac gcg			1008
Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Thr Asp Asn Ala			
325	330	335	
gat aac ctg atc gac ctt tac aag caa acg cgc gct gaa ggt ttc gga			1056
Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr Arg Ala Glu Gly Phe Gly			
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Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser			
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Gly Tyr Tyr Asp Ala Tyr Tyr Lys Ala Gln Lys Val Arg Thr Leu			
370	375	380	
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Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val			
385	390	395	400
gga ccg act aca ccg aca cct gcg ttt aaa atc ggt gaa aac acg aag			1248
Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys			
405	410	415	
gat ccg ctc aca atg tac gca aac gat atc tta acg att ccg gtc aac			1296
Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn			
420	425	430	
ctt gcg gcg tac cgg gaa tca ggt gcc atg cgg tta gca gac gga ctt			1344
Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu			
435	440	445	
ccg ctc ggc ctg caa atc atc gga aaa cac ttt gat gaa gca ctg tat			1392
Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr			
450	455	460	
acc gcg ttg ctc atg cat ttg aac aag caa cag acc atc ata aag caa			1440

Thr Ala Leu Leu Met His Leu Asn Lys Gln Gln Thr Ile Ile Lys Gln
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35 40 45

Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly
50 55 60

Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp
65 70 75 80

Asn Ile Val Thr Lys Gly Leu Arg Thr Thr Cys Ser Ser Lys Ile Leu
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Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr Val Val Gln Arg Leu Gln
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Asp Ala Glu Ala Val Thr Ile Gly Lys Leu Asn Met Asp Glu Phe Ala
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180 185 190

Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser
195 200 205

Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg Thr Val Glu Asp Asn Ala
210 215 220

Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser
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245 250 255

Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val
260 265 270

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Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val
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Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn
420 425 430

Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu
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 <223> Subunit B, corresponds to nucleotides 1876 - 3306
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 or Ser or Tyr or Cys. Xaa at amino acid 164 = Ser
 or Pro or Thr or Ala.

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 35 40 45

cct gtt ctg aac aaa gaa gcc gtt gaa ttc gca atg aaa gcc gct atg 192
 Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met
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 100 105 110

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 Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly
 115 120 125

aaa ctg acg cat acg ggc gac ggc tat tct ctt gtt gac ttc aac cgt 432
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 130 135 140

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 145 150 155 160

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165

170

175

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190																																																																																																							
gac gcc aat atc tct ctt cgt ccg atc ggc caa gag gaa ttc ggc aca	624																																																																																																						
Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr																																																																																																							
195	200	205		aaa aca gaa ttg aaa aac ttg aac tcc ttt gcg ttt gtt caa aaa ggc	672	Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly		210	215	220		ctt gag cat gaa gaa aaa cgc cag gag cag gtt ctt ctt tcc ggc ttc	720	Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe		225	230	235	240	ttc atc cag caa gaa act cgc cgt tat gat gaa gca acg aag aaa acc	768	Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr		245	250	255		att ctt atg cgt gtc aaa gag gga tct gac gac tac cgt tac ttc cca	816	Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro		260	265	270		gag cca gat cta gtc gag ctc tac att gat gat gaa tgg aag gaa cgc	864	Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg		275	280	285		gta aaa gca agc att cct gag ctt ccg gat gag cgc cgc aag cgt tat	912	Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr		290	295	300		atc gaa gag ctt ggc ttc gct gca tat gac gca atg gtt ctg acg ctg	960	Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu		305	310	315	320	aca aaa gaa atg gct gat ttc ttc gaa gaa acc gtt caa aaa ggc gct	1008	Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala		325	330	335		gaa gct aaa caa gcg tct aac tgg ctg atg ggt gaa gtg tca gct tac	1056	Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr		340	345	350		cta aac gca gaa caa aaa gag ctt gcc gat gtt gcc ctg aca cct gaa	1104	Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu		355	360	365		ggc ctt gcc ggc atg atc aaa ttg att gaa aaa gga acc att tct tct	1152	Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser		370	375	380		aag atc gcg aag aaa gtg ttt aaa gaa ttg att gaa aaa ggc ggc gac	1200	Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp									
205																																																																																																							
aaa aca gaa ttg aaa aac ttg aac tcc ttt gcg ttt gtt caa aaa ggc	672																																																																																																						
Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly																																																																																																							
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220																																																																																																							
ctt gag cat gaa gaa aaa cgc cag gag cag gtt ctt ctt tcc ggc ttc	720																																																																																																						
Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe																																																																																																							
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ttc atc cag caa gaa act cgc cgt tat gat gaa gca acg aag aaa acc	768																																																																																																						
Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr																																																																																																							
245	250	255		att ctt atg cgt gtc aaa gag gga tct gac gac tac cgt tac ttc cca	816	Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro		260	265	270		gag cca gat cta gtc gag ctc tac att gat gat gaa tgg aag gaa cgc	864	Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg		275	280	285		gta aaa gca agc att cct gag ctt ccg gat gag cgc cgc aag cgt tat	912	Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr		290	295	300		atc gaa gag ctt ggc ttc gct gca tat gac gca atg gtt ctg acg ctg	960	Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu		305	310	315	320	aca aaa gaa atg gct gat ttc ttc gaa gaa acc gtt caa aaa ggc gct	1008	Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala		325	330	335		gaa gct aaa caa gcg tct aac tgg ctg atg ggt gaa gtg tca gct tac	1056	Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr		340	345	350		cta aac gca gaa caa aaa gag ctt gcc gat gtt gcc ctg aca cct gaa	1104	Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu		355	360	365		ggc ctt gcc ggc atg atc aaa ttg att gaa aaa gga acc att tct tct	1152	Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser		370	375	380		aag atc gcg aag aaa gtg ttt aaa gaa ttg att gaa aaa ggc ggc gac	1200	Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp																																	
255																																																																																																							
att ctt atg cgt gtc aaa gag gga tct gac gac tac cgt tac ttc cca	816																																																																																																						
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270																																																																																																							
gag cca gat cta gtc gag ctc tac att gat gat gaa tgg aag gaa cgc	864																																																																																																						
Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg																																																																																																							
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atc gaa gag ctt ggc ttc gct gca tat gac gca atg gtt ctg acg ctg	960																																																																																																						
Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu																																																																																																							
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ggc ctt gcc ggc atg atc aaa ttg att gaa aaa gga acc att tct tct	1152																																																																																																						
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370	375	380		aag atc gcg aag aaa gtg ttt aaa gaa ttg att gaa aaa ggc ggc gac	1200	Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp																																																																																																	
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aag atc gcg aag aaa gtg ttt aaa gaa ttg att gaa aaa ggc ggc gac	1200																																																																																																						
Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp																																																																																																							

385	390	395	400	
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gct gag aag att gtg aaa gag aaa ggc ctt gtt cag att tct gac gaa Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu				
405	410	415		
				1296
ggc gtg ctt ctg aag ctt gtc act gag gcg ctt gac aac aat cct caa Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln				
420	425	430		
				1344
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435	440	445		
				1392
gtc gga cag att atg aaa gcg tcc aaa gga caa gcc aac ccg ccg atg Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met				
450	455	460		
				1431
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Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu				
35	40	45		
Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met				
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Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn				
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Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp				
85	90	95		
Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys				
100	105	110		

Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly
 115 120 125

 Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg
 130 135 140

 Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr
 145 150 155 160

 Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln
 165 170 175

 Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys
 180 185 190

 Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr
 195 200 205

 Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly
 210 215 220

 Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe
 225 230 235 240

 Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr
 245 250 255

 Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro
 260 265 270

 Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg
 275 280 285

 Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr
 290 295 300

 Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu
 305 310 315 320

 Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala
 325 330 335

 Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr
 340 345 350

 Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu
 355 360 365

 Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser
 370 375 380

 Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp
 385 390 395 400

 Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu
 405 410 415

Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln
420 425 430

Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu
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1 5 10 15

aga ctt gcg att act gaa gaa gca aaa atg ttc act gaa cag ctc 96
Arg Leu Ala Ile Thr Glu Glu Ala Lys Met Phe Thr Glu Gln Leu
20 25 30

gac agt atc att tca ttt gcc gag gag ctt aat gag gtt aac aca gac 144
Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp
35 40 45

aat gtg gag cct aca act cac gtg ctg aaa atg aaa aat gtc atg aga 192
Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg
50 55 60

gaa gat gaa gcg ggt aaa ggt ctt ccg gtt gag gat gtc atg aaa aat 240
Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn
65 70 75 80

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Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp
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taa 291

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Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp
35 40 45

Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg
50 55 60

Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn
65 70 75 80

Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp
85 90 95